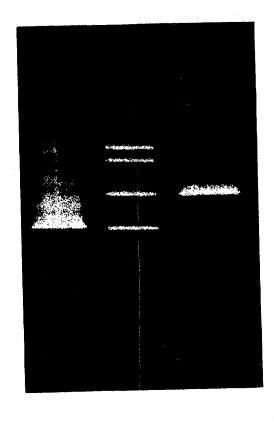


1 : Wild Type

Heterozygote Mutant



Fig. 2



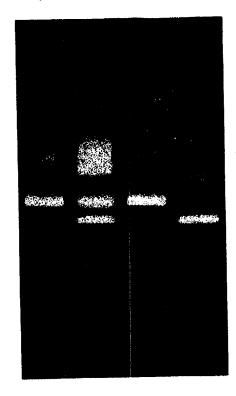
1: Wild Type

2 : Heterozygote Mutant

3 : Homozygote Mutant

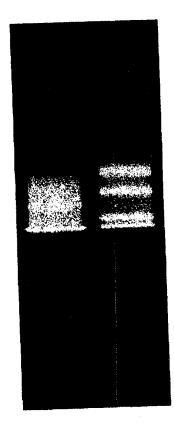


1 2 3 4



- **1**, **3**: Wild Type
- 2: Heterozygote Mutant
- 4: Homozygote Mutant



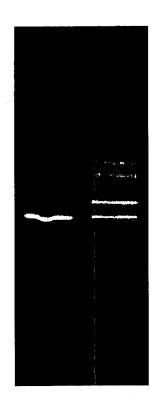


1: Wild Type

2 : Heterozygote Mutant



Fig. 5



1: Wild Type

2 : Heterozygote Mutant

Thr Gln Thr Val Pro

C 350 ACT CAG AC / GTA CCT

Maddle

Arg ValGln / AspMet Trp

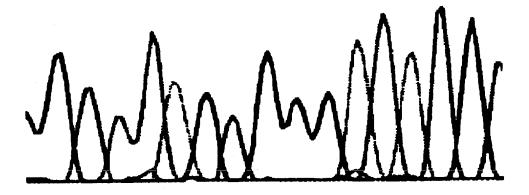
GTC CAG / GG GAC ATG

Mulman



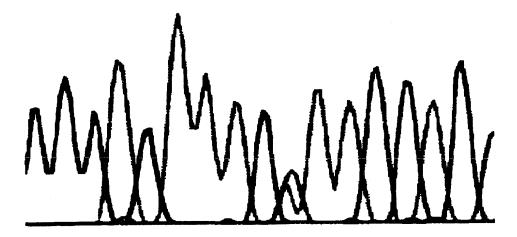
## ValGlnTrpAspMet

GTC CAG TGG GAC ATG



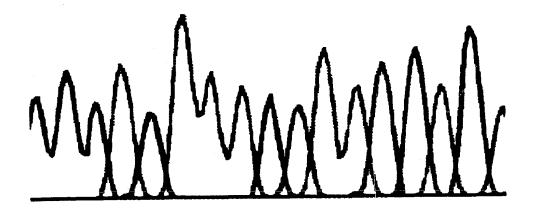
Cys Ile Asn Tyr

Å
ttag AA AT/ AAC TAT
C



Cys Ile Asn Tyr

ttag AA ATC AAC TAT



264

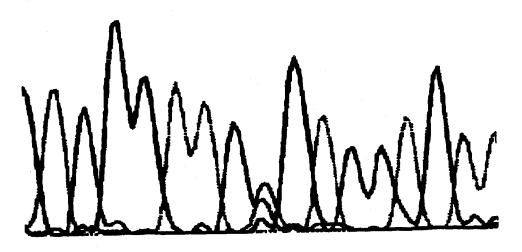
Ser LeuGlu / IleIle Leu

791

785

790**C** 795

CTG GAA T/G ATT ATA





281 Pro Asp

Fig. 12

gtotott/atttcctttttgctttgtcatag A CCT GAC a

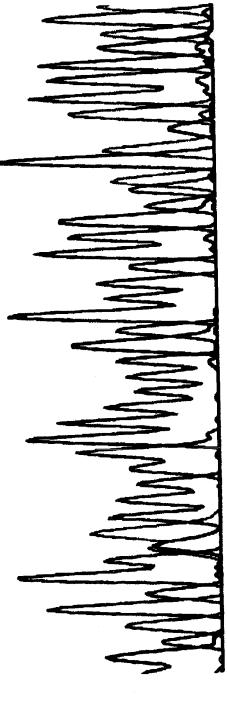
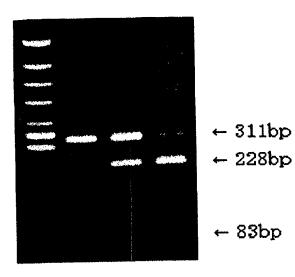




Fig. 13

M 1 2 3



M: Molecular Weight Marker

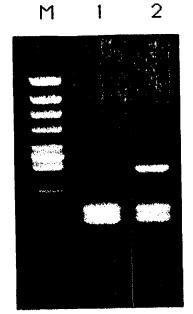
1: Wild Type

2: Heterozygote Mutant

3: Homozygote Mutant



Fig. 14



← 274bp

← 149bp ← 125bp

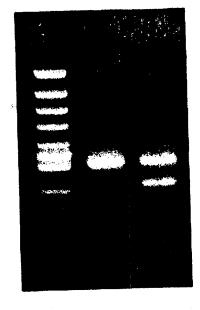
M: Molecular Weight Marker

1: Wild Type

Heterozygote Mutant



1 2 M



← 297bp

← 220bp

← 77bp

Molecular M:Weight Marker

1: Wild Type

2: Heterozygote Mutant